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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2010; month=1; day=27; hr=10; min=15; sec=52; ms=475;]

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Reviewer Comments:

1.

nbsp; Empty lines found between the amino acid numbering and the proteins SEQID (2)

E321 No. of Bases conflict, this line has no nucleotides
SEQID (2) POS (464)

E355 Empty lines found between the amino acid numbering and the proteins SEQID (2)

E321 No. of Bases conflict, this line has no nucleotides
SEQID (2) POS (464)

W112 Upper case found in data; Found at position(0) SeqId(2)

W112 Upper case found in data; Found at position(1) SeqId(2)

W112 Upper case found in data; Found at position(2) SeqId(2)

W112 Upper case found in data; Found at position(3) SeqId(2)

E259 Found undefined lettercode; POS (5) SEQID(2)

E259 Found undefined lettercode; POS (6) SEQID(2)

E259 Found undefined lettercode; POS (7) SEQID(2)

E259 Found undefined lettercode; POS (8) SEQID(2)

E259 Found undefined lettercode; POS (9) SEQID(2)

E259 Found undefined lettercode; POS (10) SEQID(2)

E259 Found undefined lettercode; POS (11) SEQID(2)

E259 Found undefined lettercode; POS (12) SEQID(2)

E259 Found undefined lettercode; POS (13) SEQID(2)

<210> 2

<211> 475

<212> PRT

<213> Homo sapiens

<220>

<223> Peptide sequence of double mutant His310-H435Lys.

<400> 2

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

4

1

WASH_6680526.1

The Sequence Listing file must end at the bottom of the last SEQ ID #.
There can be no extra information following the last SEQ ID # in the
file. Please remove extra information, "4", "1", and "WASH_6680526.1"
found at the end of the file, after SEQ ID # 2.

2.

<110> LABORATOIRE FRANÇAIS DU FRACTIONNEMENT ET DES
BIOTECHNOLOGIES

BOUREL, Dominique

GLACET, Arnaud

JORIEUX, Sylvie

STURA, Enrico

DUCANCEL, Frédéric

TEILLAUD, Jean-Luc

<120> USE OF METALLIC CATIONS TO IMPROVE FUNCTIONAL ACTIVITY
OF ANTIBODIES

<130> D 21 711 NT

<140> 10576440
<141> 2010-01-08

<150> PCT/FR2004/002687
<151> 2004-10-20

<150> FR 03 12228
<151> 2003-10-20

<160> 2

<170> PatentIn version 3.3

The sequence listing must be in ASCII text format. This file contains non-ASCII text characters, see numeric identifier <110> the accent marks in the name "Frédéric". Please make all changes necessary to convert this file to ASCII text only.

Application No: 10576440 Version No: 1.0

Input Set:**Output Set:**

Started: 2010-01-08 14:18:39.238
Finished: 2010-01-08 14:18:43.864
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 626 ms
Total Warnings: 4
Total Errors: 13
No. of SeqIDs Defined: 2
Actual SeqID Count: 2

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (2)
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E 321	No. of Bases conflict, this line has no nucleotides SEQID (2)
W 112	Upper case found in data; Found at position(0) SeqId(2)
W 112	Upper case found in data; Found at position(1) SeqId(2)
W 112	Upper case found in data; Found at position(2) SeqId(2)
W 112	Upper case found in data; Found at position(3) SeqId(2)
E 259	Found undefined lettercode; POS (5) SEQID(2)
E 259	Found undefined lettercode; POS (6) SEQID(2)
E 259	Found undefined lettercode; POS (7) SEQID(2)
E 259	Found undefined lettercode; POS (8) SEQID(2)
E 259	Found undefined lettercode; POS (9) SEQID(2)
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E 259	Found undefined lettercode; POS (11) SEQID(2)
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E 259	Found undefined lettercode; POS (13) SEQID(2)

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<212> DNA
<213> Homo sapiens

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<223> cDNA sequence of double mutant His310-435Lys

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agccgatggc tgcaattagg tcttgaagat gcttttcata tctggggcca ggggacaatg 420
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gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 960
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gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1140
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<210> 2
<211> 475
<212> PRT
<213> Homo sapiens

<220>
<223> Peptide sequence of double mutant His310-H435Lys.

<400> 2

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1 5 10 15

Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe
35 40 45

Lys Asn Tyr Ala Met His Trp Val Arg Gln Ala Pro Ala Lys Gly Leu
50 55 60

Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Arg Asn Ile Gln Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Cys Thr Phe Ser Arg Asp Asn Ser Gln Asp
85 90 95

Thr Leu Tyr Leu Gln Leu Asn Ser Leu Arg Pro Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Pro Val Arg Ser Arg Trp Leu Gln Leu Gly Leu
115 120 125

Glu Asp Ala Phe His Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
130 135 140

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
145 150 155 160

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
165 170 175

Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	180	185	190	
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	195	200	205	
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	210	215	220	
Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	225	230	235	240
Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	245	250	255	
Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	260	265	270	
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	275	280	285	
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	290	295	300	
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	305	310	315	320
Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	325	330	335	
Leu	Lys	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	340	345	350	
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	355	360	365	
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	370	375	380	
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	385	390	395	400
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu				

405

410

415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
420 425 430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
435 440 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Lys Tyr
450 455 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

4

1

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